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EXAMINER	
MYERS, CARLA J	

ART UNIT	PAPER NUMBER
1634	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/786,970	KNOLL ET AL.	
	Examiner	Art Unit	
	Carla Myers	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *3/18/08 and 7/18/08*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-12* is/are pending in the application.

4a) Of the above claim(s) *1-8,11 and 12* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *9 and 10* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

1. This action is in response to the amendments filed March 18, 2008 and July 18, 2008. Applicant's arguments have been fully considered but are not persuasive to overcome all grounds of rejection. All rejections not reiterated herein are hereby withdrawn. In particular, the objection to the specification over the presence of an embedded hyperlink has been obviated by the amendments to the specification.

This action is made final.

Election/Restrictions

2. Claims 9 and 10 are drawn to the elected invention and have been examined herein.

Claims 1-8, 11 and 12 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected invention, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on February 26, 2007.

Sequence Listing

3. The CRF copy of the Sequence Listing filed July 18, 2008 is in compliance and has been entered.

Claim Rejections - 35 USC § 112 – Written Description

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 9 and 10 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to

reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

In analyzing claims for compliance with the written description requirement of 35 U.S.C. 112, first paragraph, the written description guidelines note that with regard to genus/species situations, a "Satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (See: Federal Register: December 21, 1999 (Volume 64, Number 244), revised guidelines for written description.)

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of a complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, and any combination thereof.

Thereby, to ascertain whether the written description requirement is met for a genus claim, it is first determined whether a representative number of species have been described by their complete structure. It is then determined whether a representative number of species have been defined by other identifying characteristics. In the present situation, claim 9 is drawn to a method for developing a hybridization probe comprising determining a sequence of a single copy sequence by ascertaining

the nucleotide by nucleotide sequence of a target nucleic acid sequence, comparing the target nucleic acid sequence with known repeat sequences, identifying said single copy sequence from the comparison, and developing a hybridization probe from the non-repetitive portion of the target nucleic acid, wherein the repeat sequences appear at least 10 times in the genome and are at least about 50 nucleotides in length. Claim 10 is drawn to a method for identifying a single copy sequence interval in a target nucleic acid comprising ascertaining the nucleotide by nucleotide sequence of a target nucleic acid sequence, comparing the target nucleic acid sequence with known repeat sequences using a computer program and identifying said single copy sequence from the comparison wherein the repeat sequences appear at least 10 times in the genome and are at least about 50 nucleotides in length.

The specification discloses repeat sequences identified in the human genome and consisting of the sequences of SEQ ID NO: 1-428 and 447-479. Accordingly, the specification teaches the complete structure of the repeat sequences consisting of SEQ ID NO: 1-428 and 447-479. However, the present claims require the use of "known" repeat sequences, wherein the repeat sequences are defined only in terms of the fact that they occur at least 10 times in a genome and are at least 50 nucleotides in length. The claims do not define the "known" repeat sequences in terms of any other structural features, such as their nucleotide sequence, the sequence identity they share with other sequences, etc. Further, what constitutes a known sequence varies over time and with one's interpretation of this term. While a repeat sequence may be known to one researcher, that same repeat sequence may not be known to the general public.

Similarly a repeat sequence may be "known" in that it exists in an organism, but the actual nucleotide sequence and identity of the repeat sequence may not have been characterized. The human genome and the genome of other organisms, including all animals, plants, and microorganisms are expected to include a substantially large number of repeat sequences, differing from one in another in terms of their nucleotide sequence, length and frequency. Thereby, the disclosure of the specific sequences of SEQ ID NO: 1-428 and 447-479 is not considered to constitute a representative number of the claimed "known repeat sequences" which are not defined in terms of any relevant structural limitations.

It is then determined whether a representative number of species have been sufficiently described by other relevant identifying characteristics (e.g. restriction map, biological activity of an encoded protein product, etc.). In the present application, no additional members of the claimed genus have been described by other relevant identifying characteristics other than the length of the repeat sequence being greater than 50 nucleotides. However, this recitation does not serve to meaningfully distinguish the claimed repeat sequences over other sequences. Further, no repeat sequences have been provided that were obtained from non-human organisms, such as vertebrates, plants or microorganisms.

Additionally, the specification does not disclose a clear relationship between the structure and function of the claimed "known repeat sequences."

In the absence of a representative number of species of the claimed genus, there is insufficient descriptive support for the currently claimed genus of any "known repeat sequences" obtained from any human or any non-human organism.

The decisional law in this area has been very consistent. The Federal Circuit in Lilly, Fiers, Rochester and many other cases has determined that the written description issue applies to situations where the definition of the subject matter of the claims fails to provide description commensurate with the genus. The most recent case law directly supports this rejection. As the District Court in University of Rochester v. G.D. Searle & Co., Inc. (2003 WL 759719 W.D.N.Y.,2003. March 5, 2003.) noted "In effect, then, the '850 patent claims a method that cannot be practiced until one discovers a compound that was not in the possession of, or known to, the inventors themselves. Putting the claimed method into practice awaited someone actually discovering a necessary component of the invention." This is similar to the current situation since the breadth of the current claims comprises the use of repeat sequences which the present inventors were not in the possession of, or which were not known to the inventors. In a genus that is possibly quite immense, the specification discloses only a limited number of embodiments – that is the sequences of SEQ ID NO: 1-428 and 447-479.

As noted in Vas-Cath Inc. v. Mahurkar (19 USPQ2d 1111, CAFC 1991), the Federal Circuit concluded that:

"...applicant must also convey, with reasonable clarity to those skilled in art, that applicant, as of filing date sought, was in possession of invention, with invention being, for purposes of "written description" inquiry, whatever is presently claimed."

Applicant is reminded that *Vas-Cath* makes clear that the written description provision of 35 U.S.C. 112 is severable from its enablement provision.

This finding is also emphasized in *Ex Parte Kubin* (No. 2007-0819, Bd. Pat. App. & Int. May 31, 2007), wherein it is stated that :

"Although there is often significant overlap" between the enablement and written description requirements, "they are nonetheless independent of each other." University of Rochester, 358 F.3d at 921, 69 USPQ2d at 1891. An "invention may be enabled even though it has not been described." Id. Such is the situation here. While we conclude one skilled in the art would have been able to make and use the full scope of claim 73 through routine experimentation, we find Appellants did not describe the invention of claim 73 sufficiently to show they had possession of the claimed genus of nucleic acids. See, e.g., Noelle v. Lederman, 355 F.3d 1343, 1348, 69 USPQ2d 1508, 1513 (Fed. Cir. 2004) ("invention is, for purposes of the 'written description' inquiry, whatever is now claimed").

Further, "Possession may not be shown by merely describing how to obtain possession of members of the claimed genus or how to identify their common structural features. *See University of Rochester*, 358 F.3d at 927, 69 USPQ2d at 1895." Thereby, a showing of how to potentially identify and make other repeat sequences is not sufficient to establish that Applicant's were in possession of the invention as broadly claimed.

Accordingly, there is no record or description which would demonstrate conception of any repeat sequences from any human or non-human organism other

than those expressly disclosed as the human repeat sequences of SEQ ID NO: 1-428 and 447-479. Therefore, the claims fail to meet the written description requirement because the claims encompass a significantly large genus of polynucleotide sequences which are not described in the specification.

Response to Remarks:

In the response, Applicants state those of skill in the art know what a repeat sequence is and know where the most up-to-date listing of repeat sequences can be found. It is stated that software programs are available to derive single copy sequences. It is asserted that the repeat sequences are defined in the claims in that they occur more than 10 times in a genome and are at least 50 nucleotides in length. It is also argued that Applicants have not only described over 428 repeat sequences, but have also taught where to find future examples of repeat sequences.

These arguments have been fully considered but are not persuasive. The present rejection does not question whether one of skill in the art could identify a repeat sequence. The rejection is based on a lack of written description of a representative number of "known repeat sequences." The "known repeat sequences" are essential to accomplishing the objective of the claims of identifying a single copy sequence. The claims are not limited to methods which detect a sequence which lack only one or two of the currently known repeat sequences, or which lack the repeat sequences of SEQ ID NO: 1-428 or 447-479. Rather, the claims require the use of all known repeat sequences in order to determine that a sequence is a single copy sequence. The claims do not recite any additional active process steps for determining that the sequence is a

single copy sequence. Thereby, comparison of the target sequence to only one or two etc of the currently known repeat sequence would not result in the identification of a single copy sequence since other repeat sequences may be present in the target nucleic acid. Thus, to practice the present invention requires knowledge of the structure of the repeat sequences present in human and non-human organisms. Yet, the claims do not define the "known repeat sequences" in terms of their complete structure or in terms of other sufficient identifying characteristics. The recitations that the repeat sequences occur at least 10 times in a genome and are of at least 50 nucleotides are not sufficient to describe the overall structure of the repeat sequences and to establish that at the time of filing, Applicants were in possession of a known human and non-human repeat sequences. In fact, the present specification exemplifies only human repeat sequences. There is no evidence of record to establish that Applicants were in possession of a representative number of known repeat sequences from the vast number of non-human genomes.

As set forth in *Rochester*, 358 F.3d at 923; *Eli Lilly*, 119 at 1568, the "disclosure must allow one skilled in the art to visualize or recognize the identity of the subject matter purportedly described." *Id.* Not all functional descriptions "necessarily fail as a matter of law to meet the written description requirement; rather, the requirement may be satisfied if in the knowledge of the art the disclosed function is sufficiently correlated to a particular, known structure." *Amgen Inc. v. Hoechst Marion Roussel, Inc.*, 314 F.3d 1313, 1332 (Fed. Cir. 2003).,

However, in the present situation, the specification does not disclose a clear structure-function relationship between the sequences that are at least 50 nucleotides in length and occur 10 times in a genome and the function that the sequences are repeat sequence. No common structure has been disclosed to identify those sequences which are repeat sequences. In the absence of any real structure-function relationship and in the absence of a representative number of species of the claimed genus, there is insufficient descriptive support for the currently claimed genus of "known repeat sequences."

Further, with respect to Applicant's arguments that the specification teaches where and how to locate repeat sequences, the findings of *Ex Parte Kubin* (No. 2007-0819, Bd. Pat. App. & Int. May 31, 2007 are again noted:

"Although there is often significant overlap" between the enablement and written description requirements, "they are nonetheless independent of each other." University of Rochester, 358 F.3d at 921, 69 USPQ2d at 1891. An "invention may be enabled even though it has not been described." Id. Such is the situation here. While we conclude one skilled in the art would have been able to make and use the full scope of claim 73 through routine experimentation, we find Appellants did not describe the invention of claim 73 sufficiently to show they had possession of the claimed genus of nucleic acids. See, e.g., Noelle v. Lederman, 355 F.3d 1343, 1348, 69 USPQ2d 1508, 1513 (Fed. Cir. 2004) ("invention is, for purposes of the 'written description' inquiry, whatever is now claimed").

Applicants have asserted that the findings of *Ex parte Kubin* do not apply to the present situation because Applicants have identified over 400 repeat sequences. However, Applicants have not established that the disclosure of the approximately 428 human repeat sequences constitutes a representative number of currently known and unknown repeat sequences in human and non-human genomes. Thereby, a showing of how to potentially identify and make other "known repeat sequences" is not sufficient to establish that Applicant's were in possession of the invention as broadly claimed, which requires the genus of currently known and subsequently known human and non-human repeat sequences.

Applicants also assert that "(t)he mere fact that this may change over time as new repeat sequences are found does not detract from the fact that the present inventors have developed a method that develops probes and identifies sequences useful for probe formation. As a simplification, if an inventor provides a novel method of changing tires, and demonstrates that his method work through examples, it does not matter if new tires are developed in the future, if the tires are being changed on a Chevy, Buick, or Honda, or if the tires need to be changed in Kansas, Canada, Australia, or even a road that did not exist at the time the invention was made. If the steps of the method can still be applied, it would be unfair to the inventor to say that such new tires or the different locations for changing tires would prevent them from enjoying the full benefit of their contribution to the art. "

This argument has also been fully considered but is not persuasive. While the present method develops probes and identifies sequences for probe formation, the

claimed methods require the use of "known repeat sequences" which are not adequately described in terms of their structure. The analogy set forth by Applicants does not apply to the present claims. The rejection is not based on whether one could practice the claimed invention in another state or country. In Applicants analogy, the tire itself appears to be irrelevant to the invention of a new method of changing a tire. That is not the case herein, wherein the repeat sequence is essential to the invention. That is, the claimed method cannot be practiced without knowing the repeat sequence and what is determined to be a single copy sequence is defined by the sequence of the repeat sequence. The method of changing the tire isn't altered based on the tire itself, whereas the hybridization probe consisting of a single copy sequence will be altered depending on what is selected as the "known repeat sequences."

Applicants argue that the specification teaches how to make repeat sequences for any organism and therefore those of skill in the art are able to practice the invention to create hybridization probes regardless of their origin. This argument is also not persuasive because it is directed only to the issue of whether the specification enables one to search and identify repeat sequences in non-human organisms. However, the claims are not drawn to methods of searching for and identifying repeat sequences in non-human organisms. Rather, the claims are directed to methods which require the use of already known repeat sequences. Again, the specification does not disclose any repeat sequences obtained from non-human organisms. Thereby, the teachings in the specification as to how to identify repeat sequences in non-human organisms is not

sufficient to establish that Applicant's were in possession of the invention as broadly claimed.

Accordingly, the rejection of claims 9 and 10 under 35 U.S.C. 112, first paragraph is maintained.

Claim Rejections - 35 USC § 112 second paragraph

5. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 9 and 10 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

A. Claims 9 and 10 are indefinite over the recitation of "known repeat sequence". What constitutes a known repeat sequence varies over time, such that what repeat sequence is unknown today, may become known tomorrow. In addition, a sequence that is "unknown" to one individual (e.g., because it is not in a public database), may be known to another individual who is performing research on this sequence. Also, a repeat sequence may be known because it exists in nature, but the specific nucleotide structure or the location in a genome of the sequence may not have been characterized. Since what constitutes "known" changes over time, and may vary depending on the individual and the interpretation of what is known, there is not a fixed and complete definition for what constitutes the "known repeat sequence." Accordingly, one of skill in the art cannot determine the meets and bounds of the claimed subject matter.

Response to Remarks:

In the response, Applicants state that there will always be repeat sequences within the genome of an individual and that those of skill in the art will have the required knowledge to obtain the most accurate of the genome and therefore will be aware of where repetitive sequences lie.

These arguments have been fully considered but are not persuasive. While one might be able to search and find repeat sequences, the rejection is not based on the concept that cannot determine where a repetitive sequence lies. The rejection is based on the finding that the specification does not define what constitutes a "known repetitive sequence" and there is no art recognized definition for this term. Since what constitutes a "known repetitive sequence" will change over time and will change from individual to individual, there is no clear definition for this term. Thereby, one of skill in the art cannot determine the meets and bounds of what is intended to be encompassed by "known repeat sequences."

B. Claims 9 and 10 are indefinite over the recitation of "determining the sequence of at least one single copy sequence in said target nucleic acid computationally" (claim 9) and "identifying a single copy sequence interval from a target nucleic acid sequence computationally" (claim 10) because it is unclear as to how the recitation of "computationally" is intended to further limit the claims since the determining and identifying steps as further defined in the claims do not include the use of a computer or other numerical means.

Response to Remarks:

In the response, Applicants state that the recitation of "computationally" refers to the part of the method in which one of skill in the art would use a genome database to find and compare the appropriate repeat sequences and target sequences. This argument is not persuasive because the claims do not recite a step wherein a single copy sequence is determined computationally by using a genome database to find and compare repeat sequences and target sequences. Further, the specification does not define the term "computationally" as having such a meaning. Since the claims do not recite any particular steps of using a computer or any other numerical means to determine a single copy sequence and because the phrase "computationally" is not defined in the specification or claims as having the meaning asserted by Applicants, one of skill in the art would not know how the recitation of "computationally" is intended to further limit the claims.

Double Patenting

6. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 9 and 10 are rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-8 of U.S. Patent No.6,828,097. Although the conflicting claims are not identical, they are not patentably distinct from each other because the present claims and the claims of '097 are both inclusive of methods of developing hybridization probes and identifying a single copy sequence interval comprising determining the sequence of a single copy sequence in a target nucleic acid by ascertaining the nucleotide-by-nucleotide sequence of the target nucleic acid, comparing the ascertained sequence to known repeat sequences, identifying a single copy sequence from the comparison and developing a hybridization probe to a portion of the single-copy sequence. While the claims of '097 are limited to particular known repeat sequences, the present claims encompass any repeat sequence and thereby encompass the repeat sequences recited in '097.

Response to Remarks:

In the response, Applicants state that they will file a terminal disclaimer "upon issuance of the application if such a terminal disclaimer is still warranted."

Applicants did not specifically traverse the above rejection. The rejection is maintained for the reasons stated above.

Claim Rejections - 35 USC § 102

7. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 9 and 10 are rejected under 35 U.S.C. 102(e) as being anticipated by Kazazian et al (U.S. Patent NO. 6150160).

Kazazian (col. 42) teaches methods of identifying a single copy sequence interval and methods of developing a hybridization probe to a single copy sequence interval comprising determining the nucleotide-by-nucleotide sequence of a target nucleic acid, comparing the ascertained nucleotide sequence to repeat sequences present in databases using BLAST (i.e., a computer program), identifying single copy sequences that do not include repetitive sequences, and developing hybridization probes comprising sequences that are complementary to the non-repetitive portion of the target nucleic acid and comprising at least a portion of the single copy sequence.

Specifically, Kazazian (col. 27, lines 24-34) teaches:

"The empty sites for insertions A-D were amplified by PCR using oligonucleotide primers that flanked the insertion site. The sequence flanking each empty site was checked for repetitive sequences using the BLAST algorithm (BCM search launcher) to scan the sequences in GenBank and an EST database (Altschul, et al., 1990, J Mol. Biol. 215:403-410). Sequences in non-repetitive DNA flanking each insertion were used to design oligonucleotide probes. Those probes were used in PCR reactions with HeLa cell genomic DNA. In every case, a single band of the predicted size was amplified."

Kazazian (col. 42) further teaches:

"Southern blot analysis was carried out on the DNAS of 19-25 different individuals using probes flanking each of the newly isolated active L1s. The 5' flank of each L1 was checked for repetitive sequences by use of the BLAST (Altschul et al. 1990. *J Mol Biol.* 215: 403-410) algorithm (BCM search launcher).Single copy probes were generated by PCR and ranged from 300-600 bp."

In the method of Kazazian, the nucleotide sequences are compared to all repeat sequences present in the GenBank and EST database, which necessarily includes repeat sequences that occur within a genome at least 10 times and which are of a length of at least 50 nucleotides. For example, Kazazian teaches screening the newly identified flanking sequences containing single-copy nucleic acids for the presence of L1 sequences, which are present 30-60 times in the average diploid human genome and are of a length of greater than 50 nucleotides (col. 1, line 49-col. 2, line 10; col. 39, lines 27-40; col. 47, lines 25-42).

Response to Remarks:

In the response, Applicants state that in the method of Kazazian the probes are developed to regions that flank the isolated L1s. It is argued that, in contrast, "the probes of the present invention hybridize to single copy target sequence, not a sequence that flanks the region of interest (i.e., the single coy sequence)." It is asserted that the probes of Kazazian were not created for the same purpose or to serve the same function as the probes of the present invention, and thus are distinct.

These arguments have been fully considered but are not persuasive. First, it is noted that the present claims are not directed to probes per se, but rather are directed to a method for developing a hybridization probe for a target nucleic acid sequence and a method for identifying a single copy sequence interval. Secondly, the present claims do not recite any particular limitations which define or otherwise characterize the target sequence to which the probe hybridizes. Thus, the single copy sequence in a target nucleic acid may be any single copy sequence present in any nucleic acid. The term "target" is arbitrary and includes any sequence to which one seeks to generate a probe. While the examples provided in the specification may be directed to methods in which the probes hybridize to sequences that are distinct from the sequences flanking the L1 regions of Kazazian, there are no limitations in the claims which define the structure or function of the target sequence in order to distinguish the target sequence recited in the claims over those in the method of Kazazian. That is, the claims fail to recite any structural or functional limitations that define the "target nucleic acid sequence" and there is nothing in the claims which specifically excludes "target nucleic acid sequences" that are sequences flanking an L1 region. Accordingly, it is maintained that the methods disclosed by Kazazian anticipate the methods of claims 9 and 10.

Conclusion

THIS ACTION IS MADE FINAL. Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within

TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carla Myers whose telephone number is 571-272-0747. The examiner can normally be reached on Monday-Thursday (6:30-5:00).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached on 571-272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Carla Myers/
Primary Examiner, Art Unit 1634